Type: Invited Presentation

Final Abstract Number: 39.004
Session: Traveling Bugs, Far and Wide
Date: Saturday, April 5, 2014
Time: 15:45-17:45
Room: Room 2.60

Postgraduate training in tropical medicine: The value of on-site experience

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Medical curricula have shifted to problem based learning and from "know all" to "know how" with an emphasis on active learning and the transmission of information in a context-based manner. Post-graduate tropical medicine training on-site in the tropics is now available on 4 continents. The Gorgas Diploma Course given annually in Lima, Peru will be used to highlight the experience over the last 20 years with over 700 participants in developing an effective learning environment for its participants, using increasingly recognized principles of adult learning. An analysis of participant profiles, pedagogic approaches, and outcome measures will be provided. The benefit of this approach will be illustrated with several clinical case studies highlighting unique pedagogic benefits of an on-site patient-based approach. The frameworks of other courses given in East Africa, South Africa, and Southeast Asia will be summarized as well.

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Type: Poster Presentation

Final Abstract Number: 40.001
Session: Antibiotic Resistance
Date: Thursday, April 3, 2014
Time: 12:45-14:15
Room: Ballroom

Multi-drug resistant tuberculosis (MDR-TB) in the Free State, South Africa in 2012

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Background: The Free State (FS) province, situated in central South Africa, has a varied population with people living in rural areas (mining communities and agricultural farms), small towns as well as in urban Bloemfontein itself. The NHLS Central laboratories in Bloemfontein are the referral laboratory for susceptibility testing of MDR-TB cases for the FS province. The WHO has reported that 5.4% – 8.2% of retreatment cases in South Africa in 2012 were MDR-TB. We aimed to perform a retrospective analysis of extensive drug resistance (XDR-TB) and MDR-TB in the FS province in 2012.

Methods & Materials: Laboratory data for the year 2012 was extracted from the DISA database of the NHLS Central laboratories for specimens received at the referral laboratory from suspected and confirmed cases of *Mycobacterium tuberculosis* (MTB). These patients were diagnosed using at least one or more of the following methods: smear microscopy, MGIT culture and/or molecular methods viz. GenoType MTBDRplus line probe assay (LPA) and Xpert® MTB/RIF. Extracted data were analysed using Excel software.

Results: For the year 2012, a total of 24500 specimens were received by the referral laboartory. Of these 4024 (16.4%) were positive and the remaining 20476 (83.6%) were negative. Of the positives 347 (8.6%) were MDR-TB (resistant to RIF and INH), which included 23 (6.6%) XDR (MDR plus ofloxacin and capreomycin resistant). Resistance profiles of MDR isolates to anti-tuberculosis drugs tested is shown in the table:

Resistance profiles of MDR- and XDR-TB strains for 2012.

	RIF	INH	OFL	CAP	PYR	Total
XDR-TB	23	23	23	23	22	23
MDR-TB	27	27	27	0	27	27
MDR-TB	2	2	2	0	0	2
MDR-TB	13	13	0	13	13	13
MDR-TB	2	2	0	2	0	2
MDR-TB	131	131	0	0	131	131
MDR-TB	149	149	0	0	0	149
Total	347	347	52	38	193	347

Conclusion: The analysis of tuberculosis in the Free State Provine shows a high TB positivity of 16.4%. The MDR-TB burden was at 8.6% and this is similar to what has been reported by the WHO for retreatment cases for the whole of South Africa. The XDR rate was also high for this province at 6.6% of MDR-TB. Resistance to capreomycin was the first 2nd line drug resistance that developed in MDR-TB strains. These findings indicate the need for close monitoring of MDR-TB in the FS. While the improved diagnostic methods may detect such cases within an acceptable time frame, effective and timely treatment is key to reducing transmission in the community and thus incidence of new cases.

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Antibiotic resistant micrococcus species isolated from cattle egrets and its implications

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Background: Cattle egrets (*Ardea ibis*) are partial migrant bird species in the tropics that move briskly around cattle populations in the grazing lands or travelling with cattle along trek routes. Their distributions appear widespread especially in Sub-Saharan Africa where transhumance forms of cattle movements predominate. However, little information is available on their extensive microbial roles in the transmission of infectious diseases to domestic animals most importantly poultry and also humans. In Nigeria, poultry disease antibodies have been demonstrated in cattle egrets but no specific link has been made to any disease agent.

Commensal/ooportunistic bacteria pathogens have been implicated severally in bacteremia and knee-joint infection.

Methods & Materials: Fresh samples of feces (n = 65) were obtained from a group of invading cattle egrets (≈ 1000) on trees in Vom, Nigeria. These egrets were not deterred by efforts at tree-trimming. Samples were enriched in tryptone-soy broth and plated on MacConkey agar using standard procedures. All positive cultures were sub-cultured on cefixime-rhamnose-sorbitol MacConkey agar (selective medium) and antibiogram was carried out using diffusion disc with 7 different antibiotics.

Results: *E. coli* (n = 58) and *Micrococcus spp.* (n = 13) were isolated from the faecal material following enrichment. The pooled *E. coli* colonies were sensitive to Ciprofloxacin (+++), Chloramphenicol (+++), Streptomycin (+), Clindamycin (+) and Tetracycline (+) but was resistant to Vancomycin VA (30) and Vancomycin VA (5).The *Micrococcus spp* was sensitive to Ciprofloxacin (+++), Vancomycin VA (30) (++) and Vancomycin VA (5) (+) but resistant to Streptomycin, Clindamycin, Tetracycline and Chloramphenicol.

Conclusion: Food animal production processes in Africa is particularly opened to abuse of antibiotics with stockmen often treating their cattle without recourse to veterinarians. Since the ecology of cattle egrets and trans-humance cattle are similar with shared environment, food sources, watering points and movement patterns, it is highly likely that drugs and medicaments are also shared by these species inadvertently. While this work has shown evidence of resistant organisms in fecal materials in cattle egret, more studies will become necessary to identify the potential epidemiologic role these species pose in spreading resistant organisms to poultry and other livestock.

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Study of ceftriaxone-resistant Klebsiella spp. clinical isolates from a rural hospital in Mozambique

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Background: *Klebsiella* spp. is among the most clinically relevant enterobacteria, being increasingly reported as a cause of serious infections and has also been associated with an increasing of multidrug-resistant (MDR) strains. The β-lactams and quinolone antibiotics are used as a treatment of infections caused by *Klebsiella* spp. The emergence of extended-spectrum beta-lactamases (ESBL) is an important public health problem, particularly in low income countries where antibiotics armamentarium is limited. The aim was to characterise beta-lactams and quinolone resistance mechanisms (MQR) in clinical isolates from a rural hospital in Manhiça, Mozambique.

Methods & Materials: ESBLs and MQR were investigated among ceftriaxone non-susceptible *K. pneumoniae* clinicalisolates recovered between 2004-2009. Characterisation of beta-lactams genes bla_{CTX-M}, bla_{SHV}, bla_{OXA} and bla_{TEM} was established by PCR and sequencing. Presence of MQR, target mutations and transferable mechanisms: *aac(6')Ib-cr*, *qnrA,B,C,D,S*, *qepA*, *oqxAB*, were tested by PCR and sequencing. Epidemiological relationship were done by phylogeny, REP-PCR, pulsed field gel electrophoresis and multilocus sequence typing(MLST), while the transferability was evaluated by conjugation. Additionally, the presence of class-1 and 2 integrons was studied.

Results: A total of 19 *K. pneumoniae* were analysed. The $bla_{CTX-M-15}$ was found in 18 strains, while the remaining 1 strain presented bla_{SHV-5}. Other ESBLs were found concomitantly: bla_{SHV-2}, bla_{SHV-2A}, bla_{SHV-12} and bla_{SHV-38} genes. Additionally, other β-lactamases as bla_{TEM-1} or bla_{OXA-1} were detected. Referent to MQR: 2 *qnrB* and 6*aac(6')Ib-cr* were found, as well as,described mutations in quinolone targets. The REP-PCR showed 15 different epidemiological profiles. The MLST analysis also showed great variability of ST groups and high transferable capacity of these gens. High presence of class-1 integrons, mainly conferring resistance to thrimetroprim and streptomycin, was detected. High levels of MDR was found to the most used antibiotics in the area. Only. no resistance to carbapenems was found.

Conclusion: These strains present a high level of variation at an epidemiological level in the mechanisms of resistance to third-generation cephalosporin, with predominance of $bla_{CTX-M-15}$. While, the presence of TMQR were less important. In general, high level of antimicrobial resistance has been found in a rural hospital with limited access to third-generation cephalosporins, and broad spectrum antibiotics in general.

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Resistance to the chemotherapeutic agents of *Staphylococcus aureus* strains isolated from hospitalized patients

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Background: In the last years, the percentage of Methicillin resistance staphylococci (MRSA) increased substantially.

The objectives of the study were the identification of the Staphylococcus strains; the an tibiotic susceptibility testing of the isolates and the detection of the main antibiotic resistance phenotypes.

Methods & Materials: Species identification was achieved by standard procedures and by the automated system Vitek 2 (Biomérieux). The susceptibility to AB was performed using the Vitek 2 (Biomérieux).

Results: We included in this study 96 strains isolated from hospitalized patients in the Emergency Hospital Prof. Dr. O. Fodor Cluj-Napoca. Of all the isolates, 62,5% were *S. aureus* strains: 41.7% of the strains were MRSA and 20.8% of the strains were MSSA. MRSA were isolated from catheters (10.4%), tracheal secretions (24%), abscesses (16.7%), biliary culture (4.2%), vaginal secretions (2.1%) and pleural liquids (3.1%). The MRSA strains showed a high resistance to Tetracycline (100%) and Imipenem (35.4%), a moderate